END SEQUENCE PROFILING

ABSTRACT OF THE DISCLOSURE

The present invention provides a novel method to identify rearrangements in a test genome, *e.g.*, a tumor genome, when compared to a reference genome. This method provides major improvements over previous methods in terms of efficiency, rapidity, and cost-effectiveness. Briefly, this method involves generating or obtaining a large insert vector library from a test genome, sequencing the ends of the inserts in the library, and comparing the co-linearity of the sequenced ends in the library with corresponding sequences within a substantially-sequenced reference genome. This invention is useful for any of a number of applications, including for identifying rearrangements in tumor genomes and for determining genetic differences between closely related species as well as between different strains of the same species.